SEQUENCE LISTING

<110> Curtis, Rory A.J., Lora, Jose M.

<120> 46798, A Human Matrix Metalloprotease and
 Uses Therefore

<130> MPI2001-014P1RNM

<140> 10/050,216

<141> 2001-01-16

<150> 60/262,252

<151> 2001-01-16

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<213> Homo sapiens

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ccggctcccg gcgaagggca gcggaggagc ggcccagagc gcgcagctag ggcactggcg 180
aaaccccggg acagtccctc tccgtgcggg ggcggcgcag agcagtccca tccccgggt 240
cccgggcgcg gctgactgcc ggctggttcc ctgcgcgcag tagctccccg agccgggctg 300
caccggaggc ggcgag atg gtc gcg cgc gtc ggc ctc ctg ctg cgc gcc ctg 352
            Met Val Ala Arg Val Gly Leu Leu Leu Arg Ala Leu
            1   5   10

cag ctg cta ctg tgg ggc cac ctg gac gcc cag ccc gcg gag cgc gga 400
Gln Leu Leu Leu Trp Gly His Leu Asp Ala Gln Pro Ala Glu Arg Gly
        15   20   25

ggc cag gag ctg cgc aag gag gcg gag gca ttc cta gag aag tac gga 448
Gly Gln Glu Leu Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly
    30   35   40

tac ctc aat gaa cag gtc ccc aaa gct ccc acc tcc act cga ttc agc 496
Tyr Leu Asn Glu Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser
45   50   55   60

gat gcc atc aga gcg ttt cag tgg gtg tcc cag cta cct gtc agc ggc 544
Asp Ala Ile Arg Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly
                65   70   75

gtg ttg gac cgc gcc acc ctg cgc cag atg act cgt ccc cgc tgc ggg 592
Val Leu Asp Arg Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly
            80   85   90

gtt aca gat acc aac agt tat gcg gcc tgg gct gag agg atc agt gac 640
Val Thr Asp Thr Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp
            95   100   105

ttg ttt gct aga cac cgg acc aaa atg agg cgt aag aaa cgc ttt gca 688
Leu Phe Ala Arg His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala
        110   115   120

aag caa ggg ggc gcc ctg gcg cac gcc ttc ctg ccc cgc cgc ggc gaa 736
Lys Gln Gly Gly Ala Leu Ala His Ala Phe Leu Pro Arg Arg Gly Glu
125   130   135   140

gcg cac ttc gac caa gat gag cgc tgg tcc ctg agc cgc cgc cgc ggg 784
Ala His Phe Asp Gln Asp Glu Arg Trp Ser Leu Ser Arg Arg Arg Gly
            145   150   155

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cgc aac ctg ttc gtg gtg ctg gcg cac gag atc ggt cac acg ctt ggc   832
Arg Asn Leu Phe Val Val Leu Ala His Glu Ile Gly His Thr Leu Gly
            160             155             170

ctc acc cac tcg ccc gcg ccg cgc gcg ctc atg gcg ccc tac tac aag   880
Leu Thr His Ser Pro Ala Pro Arg Ala Leu Met Ala Pro Tyr Tyr Lys
        175             180             185

agg ctg ggc cgc gac gcg ctg ctc agc tgg gac gac gtg ctg gcc gtg   928
Arg Leu Gly Arg Asp Ala Leu Leu Ser Trp Asp Asp Val Leu Ala Val
        190             195             200

cag agc ctg tat ggg aag ccc cta ggg ggc tca gtg gcc gtc cag ctc   976
Gln Ser Leu Tyr Gly Lys Pro Leu Gly Gly Ser Val Ala Val Gln Leu
205             210             215             220

cca gga aag ctg ttc act gac ttt gag acc tgg gac tcc tac agc ccc   1024
Pro Gly Lys Leu Phe Thr Asp Phe Glu Thr Trp Asp Ser Tyr Ser Pro
            225             230             235

caa gga agg cgc cct gaa acg cag ggc cct aaa tac tgc cac tct tcc   1072
Gln Gly Arg Arg Pro Glu Thr Gln Gly Pro Lys Tyr Cys His Ser Ser
            240             245             250

ttc gat gcc atc act gta gac agg caa cag caa ctg tac att ttt aaa   1120
Phe Asp Ala Ile Thr Val Asp Arg Gln Gln Gln Leu Tyr Ile Phe Lys
            255             260             265

ggg agc cat ttc tgg gag gtg gca gct gat ggc aac gtc tca gag ccc   1168
Gly Ser His Phe Trp Glu Val Ala Ala Asp Gly Asn Val Ser Glu Pro
        270             275             280

cgt cca ctg cag gaa aga tgg gtc ggg ctg ccc ccc aac att gag gct   1216
Arg Pro Leu Gln Glu Arg Trp Val Gly Leu Pro Pro Asn Ile Glu Ala
285             290             295             300

gcg gca gtg tca ttg aat gat gga gat ttc tac ttc ttc aaa ggg ggt   1264
Ala Ala Val Ser Leu Asn Asp Gly Asp Phe Tyr Phe Phe Lys Gly Gly
                305             310             315

cga tgc tgg agg ttc cgg ggc ccc aag cca gtg tgg ggt ctc cca cag   1312
Arg Cys Trp Arg Phe Arg Gly Pro Lys Pro Val Trp Gly Leu Pro Gln
        320             325             330

ctg tgc cgg gca ggg ggc ctg ccc cgc cat cct gac gcc gcc ctc ttc   1360
Leu Cys Arg Ala Gly Gly Leu Pro Arg His Pro Asp Ala Ala Leu Phe
        335             340             345

ttc cct cct ctg cgc cgc ctc atc ctc ttc aag ggt gcc cgc tac tac   1408
Phe Pro Pro Leu Arg Arg Leu Ile Leu Phe Lys Gly Ala Arg Tyr Tyr
        350             355             360

gtg ctg gcc cga ggg gga ctg caa gtg gag ccc tac tac ccc cga agt   1456
Val Leu Ala Arg Gly Gly Leu Gln Val Glu Pro Tyr Tyr Pro Arg Ser
365             370             375             380

ctg cag gac tgg gga ggc atc cct gag gag gtc agc ggc gcc ctg ccg   1504
Leu Gln Asp Trp Gly Gly Ile Pro Glu Glu Val Ser Gly Ala Leu Pro
                385             390             395

agg ccc gat ggc tcc atc atc ttc ttc cga gat gac cgc tac tgg cgc   1552
Arg Pro Asp Gly Ser Ile Ile Phe Phe Arg Asp Asp Arg Tyr Trp Arg
            400             405             410

ctc gac cag gcc aaa ctg cag gca acc acc tcg ggc cgc tgg gcc acc   1600
Leu Asp Gln Ala Lys Leu Gln Ala Thr Thr Ser Gly Arg Trp Ala Thr
            415             420             425

gag ctg ccc tgg atg ggc tgc tgg cat gcc aac tcg ggg agc gcc ctg   1648
Glu Leu Pro Trp Met Gly Cys Trp His Ala Asn Ser Gly Ser Ala Leu
        430             435             440

ttc tgaaggcacc tcctcacctc agaaactggt ggtgctctca gggcaaaatc   1701
Phe
445

atgttcccca cccccggggc agaacccctc ttagaagcct ctgagtccct ctgcagaaga 1761
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ccgggcagca aagcctccat ctggaagtct gtctgccttt gttccttgaa gaatgcagca 1821
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aaaaggjtcc cagatccctt ggccctttcc tccgaggact tctatcctcc ccaggccttt 1941
gtttcttcgg ctaaaggtac agttcctttc aagaggtaac agcactggga tccaagcagg 2001
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tcaggacaca gagtgggtagg gagactgatg caggcctacc agtccctggc tttttgtctg 2241
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<212> PRT
<213> Homo sapiens

<400> 2
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            20                  25                  30
Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly Tyr Leu Asn Glu
        35                  40                  45
Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser Asp Ala Ile Arg
    50                  55                  60
Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly Val Leu Asp Arg
65                  70                  75                  80
Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly Val Thr Asp Thr
                85                  90                  95
Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp Leu Phe Ala Arg
            100                 105                 110
His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala Lys Gln Gly Gly
        115                 120                 125
Ala Leu Ala His Ala Phe Leu Pro Arg Arg Gly Glu Ala His Phe Asp
    130                 135                 140
Gln Asp Glu Arg Trp Ser Leu Ser Arg Arg Arg Gly Arg Asn Leu Phe
145                 150                 155                 160
Val Val Leu Ala His Glu Ile Gly His Thr Leu Gly Leu Thr His Ser
                165                 170                 175
Pro Ala Pro Arg Ala Leu Met Ala Pro Tyr Tyr Lys Arg Leu Gly Arg
            180                 185                 190
Asp Ala Leu Leu Ser Trp Asp Asp Val Leu Ala Val Gln Ser Leu Tyr
        195                 200                 205
Gly Lys Pro Leu Gly Gly Ser Val Ala Val Gln Leu Pro Gly Lys Leu
    210                 215                 220
Phe Thr Asp Phe Glu Thr Trp Asp Ser Tyr Ser Pro Gln Gly Arg Arg
225                 230                 235                 240
Pro Glu Thr Gln Gly Pro Lys Tyr Cys His Ser Ser Phe Asp Ala Ile
                245                 250                 255
Thr Val Asp Arg Gln Gln Gln Leu Tyr Ile Phe Lys Gly Ser His Phe
            260                 265                 270
Trp Glu Val Ala Ala Asp Gly Asn Val Ser Glu Pro Arg Pro Leu Gln
        275                 280                 285
Glu Arg Trp Val Gly Leu Pro Pro Asn Ile Glu Ala Ala Ala Val Ser
    290                 295                 300
Leu Asn Asp Gly Asp Phe Tyr Phe Phe Lys Gly Gly Arg Cys Trp Arg
305                 310                 315                 320
Phe Arg Gly Pro Lys Pro Val Trp Gly Leu Pro Gln Leu Cys Arg Ala
                325                 330                 335
Gly Gly Leu Pro Arg His Pro Asp Ala Ala Leu Phe Phe Pro Pro Leu
            340                 345                 350
Arg Arg Leu Ile Leu Phe Lys Gly Ala Arg Tyr Tyr Val Leu Ala Arg
        355                 360                 365
Gly Gly Leu Gln Val Glu Pro Tyr Tyr Pro Arg Ser Leu Gln Asp Trp
    370                 375                 380
Gly Gly Ile Pro Glu Glu Val Ser Gly Ala Leu Pro Arg Pro Asp Gly
385                 390                 395                 400
Ser Ile Ile Phe Phe Arg Asp Asp Arg Tyr Trp Arg Leu Asp Gln Ala
                405                 410                 415
Lys Leu Gln Ala Thr Thr Ser Gly Arg Trp Ala Thr Glu Leu Pro Trp
            420                 425                 430
Met Gly Cys Trp His Ala Asn Ser Gly Ser Ala Leu Phe
            435                 440                 445
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<211> 1335
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<212> DNA
<213> Homo sapiens

<220>
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1   5   10   15

tgg ggc cac ctg gac gcc cag ccc gcg gag cgc gga ggc cag gag ctg   96
Trp Gly His Leu Asp Ala Gln Pro Ala Glu Arg Gly Gly Gln Glu Leu
                20   25   30

cgc aag gag gcg gag gca ttc cta gag aag tac gga tac ctc aat gaa   144
Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly Tyr Leu Asn Glu
            35   40   45

cag gtc ccc aaa gct ccc acc tcc act cga ttc agc gat gcc atc aga   192
Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser Asp Ala Ile Arg
        50   55   60

gcg ttt cag tgg gtg tcc cag cta cct gtc agc ggc gtg ttg gac cgc   240
Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly Val Leu Asp Arg
65   70   75   80

gcc acc ctg cgc cag atg act cgt ccc cgc tgc ggg gtt aca gat acc   288
Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly Val Thr Asp Thr
                85   90   95

aac agt tat gcg gcc tgg gct gag agg atc agt gac ttg ttt gct aga   336
Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp Leu Phe Ala Arg
            100   105   110

cac cgg acc aaa atg agg cgt aag aaa cgc ttt gca aag caa ggg ggc   384
His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala Lys Gln Gly Gly
            115   120   125

gcc ctg gcg cac gcc ttc ctg ccc cgc cgc ggc gaa gcg cac ttc gac   432
Ala Leu Ala His Ala Phe Leu Pro Arg Arg Gly Glu Ala His Phe Asp
        130   135   140

caa gat gag cgc tgg tcc ctg agc cgc cgc cgc ggg cgc aac ctg ttc   480
Gln Asp Glu Arg Trp Ser Leu Ser Arg Arg Arg Gly Arg Asn Leu Phe
145   150   155   160

gtg gtg ctg gcg cac gag atc ggt cac acg ctt ggc ctc acc cac tcg   528
Val Val Leu Ala His Glu Ile Gly His Thr Leu Gly Leu Thr His Ser
                165   170   175

ccc gcg ccg cgc gcg ctc atg gcg ccc tac tac aag agg ctg ggc cgc   576
Pro Ala Pro Arg Ala Leu Met Ala Pro Tyr Tyr Lys Arg Leu Gly Arg
                180   185   190

gac gcg ctg ctc agc tgg gac gac gtg ctg gcc gtg cag agc ctg tat   624
Asp Ala Leu Leu Ser Trp Asp Asp Val Leu Ala Val Gln Ser Leu Tyr
            195   200   205

ggg aag ccc cta ggg ggc tca gtg gcc gtc cag ctc cca gga aag ctg   672
Gly Lys Pro Leu Gly Gly Ser Val Ala Val Gln Leu Pro Gly Lys Leu
            210   215   220

ttc act gac ttt gag acc tgg gac tcc tac agc ccc caa gga agg cgc   720
Phe Thr Asp Phe Glu Thr Trp Asp Ser Tyr Ser Pro Gln Gly Arg Arg
225   230   235   240

cct gaa acg cag ggc cct aaa tac tgc cac tct tcc ttc gat gcc atc   768
Pro Glu Thr Gln Gly Pro Lys Tyr Cys His Ser Ser Phe Asp Ala Ile
                245   250   255

act gta gac agg caa cag caa ctg tac att ttt aaa ggg agc cat ttc   816
Thr Val Asp Arg Gln Gln Gln Leu Tyr Ile Phe Lys Gly Ser His Phe
            260   265   270

tgg gag gtg gca gct gat ggc aac gtc tta gag ccc cgt cca ctg cag   864
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Trp Glu Val Ala Ala Asp Gly Asn Val Ser Glu Pro Arg Pro Leu Gln
    275                 280                 285

gaa aga tgg gtc ggg ctg ccc ccc aac att gag gct gcg gca gtg tca   912
Glu Arg Trp Val Gly Leu Pro Pro Asn Ile Glu Ala Ala Ala Val Ser
    290                 295                 300

ttg aat gat gga gat ttc tac ttc ttc aaa ggg ggt cga tgc tgg agg   960
Leu Asn Asp Gly Asp Phe Tyr Phe Phe Lys Gly Gly Arg Cys Trp Arg
305                 310                 315                 320

ttc cgg ggc ccc aag cca gtg tgg ggt ctc cca cag ctg tgc cgg gca  1008
Phe Arg Gly Pro Lys Pro Val Trp Gly Leu Pro Gln Leu Cys Arg Ala
                325                 330                 335

ggg ggc ctg ccc cgc cat cct gac gcc gcc ctc ttc ttc cct cct ctg  1056
Gly Gly Leu Pro Arg His Pro Asp Ala Ala Leu Phe Phe Pro Pro Leu
                340                 345                 350

cgc cgc ctc atc ctc ttc aag ggt gcc cgc tac tac gtg ctg gcc cga  1104
Arg Arg Leu Ile Leu Phe Lys Gly Ala Arg Tyr Tyr Val Leu Ala Arg
                355                 360                 365

ggg gga ctg caa gtg gag ccc tac tac ccc cga agt ctg cag gac tgg  1152
Gly Gly Leu Gln Val Glu Pro Tyr Tyr Pro Arg Ser Leu Gln Asp Trp
    370                 375                 380

gga ggc atc cct gag gag gtc agc ggc gcc ctg ccg agg ccc gat ggc  1200
Gly Gly Ile Pro Glu Glu Val Ser Gly Ala Leu Pro Arg Pro Asp Gly
385                 390                 395                 400

tcc atc atc ttc ttc cga gat gac cgc tac tgg cgc ctc gac cag gcc  1248
Ser Ile Ile Phe Phe Arg Asp Asp Arg Tyr Trp Arg Leu Asp Gln Ala
                405                 410                 415

aaa ctg cag gca acc acc tcg ggc cgc tgg gcc acc gag ctg ccc tgg  1296
Lys Leu Gln Ala Thr Thr Ser Gly Arg Trp Ala Thr Glu Leu Pro Trp
                420                 425                 430

atg ggc tgc tgg cat gcc aac tcg ggg agc gcc ctg ttc             1335
Met Gly Cys Trp His Ala Asn Ser Gly Ser Ala Leu Phe
                435                 440                 445
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<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus

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Thr Arg Lys Lys Ala Ser Asn Ser Leu Val Glu Lys Leu Lys Glu Met
            20              25              30
Gln Lys Phe Phe Gly Leu Pro Val Thr Gly Lys Leu Asp Ser Asn Thr
        35              40              45
Leu Glu Val Met Lys Lys Pro Arg Cys Gly Val Pro Asp Val Gly Glu
    50              55              60
Phe Arg Thr Phe Pro Gly Ser Pro Lys Trp Ser Lys Asn Asn Leu Leu
65              70              75              80
Thr Tyr Arg Ile Val Asn Tyr Thr Pro Asp Leu Pro Arg Glu Asp Val
            85              90              95
Asp Asp Ala Ile Arg Arg Ala Phe Gln Val Trp Ser Asp Val Thr Pro
            100             105             110
Leu Thr Phe Thr Arg Val Ser Asp Gly Glu Ala Asp Ile Met Ile Ser
    115             120             125
Phe Ala Arg Gly Glu His Gly Asp Phe Tyr Pro Phe Asp Gly Lys Gly
    130             135             140
Gly Leu Leu Ala His Ala Phe Ala Pro Gly Pro Gly Ile Gly Ile Gly
145             150             155             160
Asp Ala His Phe Asp Asp Asp Glu Thr Trp Thr
                165             170
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<210> 5
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus

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Ile Asp Ala Ala Phe Glu Asp Arg Asp Arg Gly Lys Thr Tyr Phe Phe
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Lys Gly Asp Lys Tyr Trp Arg Phe Asp Pro Glu Thr Arg Gln Arg Val
            20   25   30
Asp Pro Gly Tyr Pro Lys Leu Ile Ser Asp Leu Trp Pro Asp Gly Leu
        35   40   45
Pro Cys
    50

<210> 6
<211> 471
<212> PRT
<213> Homo sapiens

<400> 6
Met His Pro Gly Val Leu Ala Ala Phe Leu Phe Leu Ser Trp Thr His
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Cys Arg Ala Leu Pro Leu Pro Ser Gly Gly Asp Glu Asp Asp Leu Ser
            20   25   30
Glu Glu Asp Leu Gln Phe Ala Glu Arg Tyr Leu Arg Ser Tyr Tyr His
        35   40   45
Pro Thr Asn Leu Ala Gly Ile Leu Lys Glu Asn Ala Ala Ser Ser Met
        50   55   60
Thr Glu Arg Leu Arg Glu Met Gln Ser Phe Phe Gly Leu Glu Val Thr
65   70   75   80
Gly Lys Leu Asp Asp Asn Thr Leu Asp Val Met Lys Lys Pro Arg Cys
            85   90   95
Gly Val Pro Asp Val Gly Glu Tyr Asn Val Phe Pro Arg Thr Leu Lys
            100   105   110
Trp Ser Lys Met Asn Leu Thr Tyr Arg Ile Val Asn Tyr Thr Pro Asp
        115   120   125
Met Thr His Ser Glu Val Glu Lys Ala Phe Lys Lys Ala Phe Lys Val
    130   135   140
Trp Ser Asp Val Thr Pro Leu Asn Phe Thr Arg Leu His Asp Gly Ile
145   150   155   160
Ala Asp Ile Met Ile Ser Phe Gly Ile Lys Glu His Gly Asp Phe Tyr
                165   170   175
Pro Phe Asp Gly Pro Ser Gly Leu Leu Ala His Ala Phe Pro Pro Gly
            180   185   190
Pro Asn Tyr Gly Gly Asp Ala His Phe Asp Asp Asp Glu Thr Trp Thr
        195   200   205
Ser Ser Ser Lys Gly Tyr Asn Leu Phe Leu Val Ala Ala His Glu Phe
    210   215   220
Gly His Ser Leu Gly Leu Asp His Ser Lys Asp Pro Gly Ala Leu Met
225   230   235   240
Phe Pro Ile Tyr Thr Tyr Thr Gly Lys Ser His Phe Met Leu Pro Asp
                245   250   255
Asp Asp Val Gln Gly Ile Gln Ser Leu Tyr Gly Pro Gly Asp Glu Asp
            260   265   270
Pro Asn Pro Lys His Pro Lys Thr Pro Asp Lys Cys Asp Pro Ser Leu
        275   280   285
Ser Leu Asp Ala Ile Thr Ser Leu Arg Gly Glu Thr Met Ile Phe Lys
    290   295   300
Asp Arg Phe Phe Trp Arg Leu His Pro Gln Gln Val Asp Ala Glu Leu
305   310   315   320
Phe Leu Thr Lys Ser Phe Trp Pro Glu Leu Pro Asn Arg Ile Asp Ala
                325   330   335
Ala Tyr Glu His Pro Ser His Asp Leu Ile Phe Ile Phe Arg Gly Arg
            340   345   350
Lys Phe Trp Ala Leu Asn Gly Tyr Asp Ile Leu Glu Gly Tyr Pro Lys
        355   360   365
Lys Ile Ser Glu Leu Gly Leu Pro Lys Glu Val Lys Lys Ile Ser Ala
    370   375   380
Ala Val His Phe Glu Asp Thr Gly Lys Thr Leu Leu Phe Ser Gly Asn
385   390   395   400
Gln Val Trp Arg Tyr Asp Asp Thr Asn His Ile Met Asp Lys Asp Tyr
                405   410   415

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Pro Arg Leu Ile Glu Glu Asp Phe Pro Gly Ile Gly Asp Lys Val Asp
        420                 425                 430
Ala Val Tyr Glu Lys Asn Gly Tyr Ile Tyr Phe Phe Asn Gly Pro Ile
        435                 440                 445
Gln Phe Glu Tyr Ser Ile Trp Ser Asn Arg Ile Val Arg Val Met Pro
    450                 455                 460
Ala Asn Ser Ile Leu Trp Cys
455                 470


<210> 7
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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<223> Xaa = A, E, Q, D, N, L, G, K, S, V, R, T, P, I,
      M, F, Y, C, W, or H.

<223> Xaa = A, E, Q, D, N, L, G, K, S, V, R, T, P, I,
      M, F, Y, C, W, or H.

<221> VARIANT
<222> (6)...(6)
<223> Xaa = L, I, V, M, Y, or W.

<221> VARIANT
<222> (7)...(7)
<223> Xaa = A, Q, N, L, G, S, V, T, I, M, F, Y, C, or W.

<221> VARIANT
<222> (9)...(9)
<223> Xaa = A, E, Q, D, N, L, G, K, S, V, R, T, P, I,
      M, F, Y, C, W, or H.

<221> VARIANT
<222> (10)...(10)
<223> Xaa = L, I, V, M, F, Y, W, G, S, P, or O.


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Xaa Xaa Xaa His Glu Xaa Xaa His Xaa Xaa
1               5                   10


<210> 8
<211> 2527
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (300)...(1859)

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gcggacccgc gggcaggcac tgcccgggct ggacgacgtc tggccggctc ccggcgaagg  120
gcagcggagg agcggcccag agcgcgcagc tagggcactg gcgaaacccc gggacagtcc  180
ctctccgtgc gggggcggcg cagagcagtc ccatccccgg ggtcccgggc gcggctgact  240
gccggctggt tccctgcgcg cagtagctcc ccgagccggg ctgcaccgga ggcggcgag   299
atg gtc gcg cgc gtc ggc ctc ctg ctg cgc gcc ctg cag ctg cta ctg  347
Met Val Ala Arg Val Gly Leu Leu Leu Arg Ala Leu Gln Leu Leu Leu
1               5                   10                  15

tgg ggc cac ctg gac gcc cag ccc gcg gag cgc gga ggc cag gag ctg  395
Trp Gly His Leu Asp Ala Gln Pro Ala Glu Arg Gly Gly Gln Glu Leu
                20                  25                  30

cgc aag gag gcg gag gca ttc cta gag aag tac gga tac ctc aat gaa  443
Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly Tyr Leu Asn Glu
        35                  40                  45
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cag gtc ccc aaa gct ccc acc tcc act cga ttc agc gat gcc atc aga    491
Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser Asp Ala Ile Arg
     50          55              60

gcg ttt cag tgg gtg tcc cag cta cct gtc agc ggc gtg ttg gac cgc    539
Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly Val Leu Asp Arg
 65          70              75              80

gcc acc ctg cgc cag atg act cgt ccc cgc tgc ggg gtt aca gat acc    587
Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly Val Thr Asp Thr
                 85              90              95

aac agt tat gcg gcc tgg gct gag agg atc agt gac ttg ttt gct aga    635
Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp Leu Phe Ala Arg
             100             105             110

cac cgg acc aaa atg agg cgt aag aaa cgc ttt gca aag caa ggt aac    683
His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala Lys Gln Gly Asn
             115             120             125

aaa tgg tac aag cag cac ctc tcc tac cgc ctg gtg aac tgg cct gag    731
Lys Trp Tyr Lys Gln His Leu Ser Tyr Arg Leu Val Asn Trp Pro Glu
     130             135             140

cat ctg ccg gag ccg gca gtt cgg ggc gcc gtg cgc gcc gcc ttc cag    779
His Leu Pro Glu Pro Ala Val Arg Gly Ala Val Arg Ala Ala Phe Gln
145             150             155             160

ttg tgg agc aac gtc tca gcg ctg gag ttc tgg gag gcc cca gcc aca    827
Leu Trp Ser Asn Val Ser Ala Leu Glu Phe Trp Glu Ala Pro Ala Thr
                 165             170             175

ggc ccc gct gac atc cgg ctc acc ttc ttc caa ggg gac cac aac gat    875
Gly Pro Ala Asp Ile Arg Leu Thr Phe Phe Gln Gly Asp His Asn Asp
             180             185             190

ggg ctg ggc aat gcc ttt gat ggc cca ggg ggc gcc ctg gcg cac gcc    923
Gly Leu Gly Asn Ala Phe Asp Gly Pro Gly Gly Ala Leu Ala His Ala
             195             200             205

ttc ctg ccc cgc cgc ggc gaa gcg cac ttc gac caa gat gag cgc tgg    971
Phe Leu Pro Arg Arg Gly Glu Ala His Phe Asp Gln Asp Glu Arg Trp
     210             215             220

tcc ctg agc cgc cgc cgc ggg cgc aac ctg ttc gtg gtg ctg gcg cac   1019
Ser Leu Ser Arg Arg Arg Gly Arg Asn Leu Phe Val Val Leu Ala His
225             230             235             240

gag atc ggt cac acg ctt ggc ctc acc cac tcg ccc gcg ccg cgc gcg   1067
Glu Ile Gly His Thr Leu Gly Leu Thr His Ser Pro Ala Pro Arg Ala
                 245             250             255

ctc atg gcg ccc tac tac aag agg ctg ggc cgc gac gcg ctg ctc agc   1115
Leu Met Ala Pro Tyr Tyr Lys Arg Leu Gly Arg Asp Ala Leu Leu Ser
                 260             265             270

tgg gac gac gtg ctg gcc gtg cag agc ctg tat ggg aag ccc cta ggg   1163
Trp Asp Asp Val Leu Ala Val Gln Ser Leu Tyr Gly Lys Pro Leu Gly
             275             280             285

ggc tca gtg gcc gtc cag ctc cca gga aag ctg ttc act gac ttt gag   1211
Gly Ser Val Ala Val Gln Leu Pro Gly Lys Leu Phe Thr Asp Phe Glu
             290             295             300

acc tgg gac tcc tac agc ccc caa gga agg cgc cct gaa acg cag ggc   1259
Thr Trp Asp Ser Tyr Ser Pro Gln Gly Arg Arg Pro Glu Thr Gln Gly
305             310             315             320

cct aaa tac tgc cac tct tcc ttc gat gcc atc act gta gac agg caa   1307
Pro Lys Tyr Cys His Ser Ser Phe Asp Ala Ile Thr Val Asp Arg Gln
                 325             330             335

cag caa ctg tac att ttt aaa ggg agc cat ttc tgg gag gtg gca gct   1355
Gln Gln Leu Tyr Ile Phe Lys Gly Ser His Phe Trp Glu Val Ala Ala
             340             345             350

gat ggc aac gtc tca gag ccc cgt cca ctg cag gaa aga tgg gtc ggg   1403
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Asp Gly Asn Val Ser Glu Pro Arg Pro Leu Gln Glu Arg Trp Val Gly
        355                 360                 365

ctg ccc ccc aac att gag gct gcg gca gtg tca ttg aat gat gga gat    1451
Leu Pro Pro Asn Ile Glu Ala Ala Ala Val Ser Leu Asn Asp Gly Asp
        370             375                 380

ttc tac ttc ttc aaa ggg ggt cga tgc tgg agg ttc cgg ggc ccc aag    1499
Phe Tyr Phe Phe Lys Gly Gly Arg Cys Trp Arg Phe Arg Gly Pro Lys
385                 390                 395                 400

cca gtg tgg ggt ctc cca cag ctg tgc cgg gca ggg ggc ctg ccc cgc    1547
Pro Val Trp Gly Leu Pro Gln Leu Cys Arg Ala Gly Gly Leu Pro Arg
                405                 410                 415

cat cct gac gcc gcc ctc ttc ttc cct cct ctg cgc cgc ctc atc ctc    1595
His Pro Asp Ala Ala Leu Phe Phe Pro Pro Leu Arg Arg Leu Ile Leu
                420                 425                 430

ttc aag ggt gcc cgc tac tac gtg ctg gcc cga ggg gga ctg caa gtg    1643
Phe Lys Gly Ala Arg Tyr Tyr Val Leu Ala Arg Gly Gly Leu Gln Val
                435                 440                 445

gag ccc tac tac ccc cga agt ctg cag gac tgg gga ggc atc cct gag    1691
Glu Pro Tyr Tyr Pro Arg Ser Leu Gln Asp Trp Gly Gly Ile Pro Glu
        450                 455                 460

gag gtc agc ggc gcc ctg ccg agg ccc gat ggc tcc atc atc ttc ttc    1739
Glu Val Ser Gly Ala Leu Pro Arg Pro Asp Gly Ser Ile Ile Phe Phe
465                 470                 475                 480

cga gat gac cgc tac tgg cgc ctc gac cag gcc aaa ctg cag gca acc    1787
Arg Asp Asp Arg Tyr Trp Arg Leu Asp Gln Ala Lys Leu Gln Ala Thr
                485                 490                 495

acc tcg ggc cgc tgg gcc acc gag ctg ccc tgg atg ggc tgc tgg cat    1835
Thr Ser Gly Arg Trp Ala Thr Glu Leu Pro Trp Met Gly Cys Trp His
                500                 505                 510

gcc aac tcg ggg agc gcc ctg ttc tgaaggcacc tcctcacctc agaaactggt    1889
Ala Asn Ser Gly Ser Ala Leu Phe
                515                 520

ggtgctctca gggcaaaatc atgttcccca ccccgggggc agaacccctc ttagaagcct    1949
ctgagtccct ctgcagaaga ccgggcagca aagcctccat ctggaagtct gtctgccttt    2009
gttccttgaa gaatgcagca ttgtctttgt ctgtccccac cacatggagg tgggggtggg    2069
atcaatctta ggaaaagcaa aaaagggtcc cagatccctt ggcccttttcc tccgaggact    2129
tctatcctcc ccaggccttt gttttttcgg ctaaaggtac agttcctttc aagaggtaac    2189
agcactggga tccaagcagg gggatgaaaa actcagcaga gaaattcgag accattttgc    2249
aagactgtgc ccttctcctc aggacccccct ggctcagttc ttgaaaaacg gtgtcatatt    2309
tagtcagagg ccccacccc aggaagcatg gatggggatg aaggcacagg cgtctccaac    2369
ctcaaaggcc ctttgtgggg tcaggacaca gagtgggagg gagactgatg caggcctacc    2429
agtccctggc tttttgtctg gggctggaat aaagaggtgc cttcagctgg tgggccgaga    2489
ggcaggaagc agccttcctt ggaaaaaaaa aaaaaaaa                          2527

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<211> 520
<212> PRT
<213> Homo sapiens

<400> 9
Met Val Ala Arg Val Gly Leu Leu Leu Arg Ala Leu Gln Leu Leu Leu
1               5                   10                  15
Trp Gly His Leu Asp Ala Gln Pro Ala Glu Arg Gly Gly Gln Glu Leu
                20                  25                  30
Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly Tyr Leu Asn Glu
        35                  40                  45
Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser Asp Ala Ile Arg
        50                  55                  60
Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly Val Leu Asp Arg
65                  70                  75                  80
Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly Val Thr Asp Thr
                85                  90                  95
Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp Leu Phe Ala Arg
        100                 105                 110
His Arg Thr Lys Met Arg Arg Lys Arg Phe Ala Lys Gln Gly Asn
        115                 120                 125
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Lys Trp Tyr Lys Gln His Leu Ser Tyr Arg Leu Val Asn Trp Pro Glu
    130                     135                     140
His Leu Pro Glu Pro Ala Val Arg Gly Ala Val Arg Ala Ala Phe Gln
145                     150                     155                 160
Leu Trp Ser Asn Val Ser Ala Leu Glu Phe Trp Glu Ala Pro Ala Thr
                    165                     170                     175
Gly Pro Ala Asp Ile Arg Leu Thr Phe Phe Gln Gly Asp His Asn Asp
                180                     185                     190
Gly Leu Gly Asn Ala Phe Asp Gly Pro Gly Gly Ala Leu Ala His Ala
            195                     200                     205
Phe Leu Pro Arg Arg Gly Glu Ala His Phe Asp Gln Asp Glu Arg Trp
    210                     215                     220
Ser Leu Ser Arg Arg Arg Gly Arg Asn Leu Phe Val Val Leu Ala His
225                     230                     235                 240
Glu Ile Gly His Thr Leu Gly Leu Thr His Ser Pro Ala Pro Arg Ala
                    245                     250                     255
Leu Met Ala Pro Tyr Tyr Lys Arg Leu Gly Arg Asp Ala Leu Leu Ser
                260                     265                     270
Trp Asp Asp Val Leu Ala Val Gln Ser Leu Tyr Gly Lys Pro Leu Gly
            275                     280                     285
Gly Ser Val Ala Val Gln Leu Pro Gly Lys Leu Phe Thr Asp Phe Glu
    290                     295                     300
Thr Trp Asp Ser Tyr Ser Pro Gln Gly Arg Arg Pro Glu Thr Gln Gly
305                     310                     315                 320
Pro Lys Tyr Cys His Ser Ser Phe Asp Ala Ile Thr Val Asp Arg Gln
                325                     330                     335
Gln Gln Leu Tyr Ile Phe Lys Gly Ser His Phe Trp Glu Val Ala Ala
                340                     345                     350
Asp Gly Asn Val Ser Glu Pro Arg Pro Leu Gln Glu Arg Trp Val Gly
            355                     360                     365
Leu Pro Pro Asn Ile Glu Ala Ala Ala Val Ser Leu Asn Asp Gly Asp
    370                     375                     380
Phe Tyr Phe Phe Lys Gly Gly Arg Cys Trp Arg Phe Arg Gly Pro Lys
385                     390                     395                 400
Pro Val Trp Gly Leu Pro Gln Leu Cys Arg Ala Gly Gly Leu Pro Arg
                405                     410                     415
His Pro Asp Ala Ala Leu Phe Phe Pro Pro Leu Arg Arg Leu Ile Leu
                420                     425                     430
Phe Lys Gly Ala Arg Tyr Tyr Val Leu Ala Arg Gly Gly Leu Gln Val
            435                     440                     445
Glu Pro Tyr Tyr Pro Arg Ser Leu Gln Asp Trp Gly Gly Ile Pro Glu
    450                     455                     460
Glu Val Ser Gly Ala Leu Pro Arg Pro Asp Gly Ser Ile Ile Phe Phe
465                     470                     475                 480
Arg Asp Asp Arg Tyr Trp Arg Leu Asp Gln Ala Lys Leu Gln Ala Thr
                    485                     490                     495
Thr Ser Gly Arg Trp Ala Thr Glu Leu Pro Trp Met Gly Cys Trp His
                500                     505                     510
Ala Asn Ser Gly Ser Ala Leu Phe
            515                     520
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<210> 10
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Met Val Ala Arg Val Gly Leu Leu Leu Arg Ala Leu Gln Leu Leu Leu
1                   5                   10                  15

tgg ggc cac ctg gac gcc cag ccc gcg gag cgc gga ggc cag gag ctg      96
Trp Gly His Leu Asp Ala Gln Pro Ala Glu Arg Gly Gly Gln Glu Leu
                20                  25                  30

cgc aag gag gcg gag gca ttc cta gag aag tac gga tac ctc aat gaa     144
Arg Lys Glu Ala Glu Ala Phe Leu Glu Lys Tyr Gly Tyr Leu Asn Glu
            35                  40                  45

cag gtc ccc aaa gct ccc acc tcc act cga ttc agc gat gcc atc aga     192
Gln Val Pro Lys Ala Pro Thr Ser Thr Arg Phe Ser Asp Ala Ile Arg
        50                  55                  60
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```
gcg ttt cag tgg gtg tcc cag cta cct gtc agc ggc gtg ttg gac cgc    240
Ala Phe Gln Trp Val Ser Gln Leu Pro Val Ser Gly Val Leu Asp Arg
65                  70                  75                  80

gcc acc ctg cgc cag atg act cgt ccc cgc tgc ggg gtt aca gat acc    288
Ala Thr Leu Arg Gln Met Thr Arg Pro Arg Cys Gly Val Thr Asp Thr
                85                  90                  95

aac agt tat gcg gcc tgg gct gag agg atc agt gac ttg ttt gct aga    336
Asn Ser Tyr Ala Ala Trp Ala Glu Arg Ile Ser Asp Leu Phe Ala Arg
            100                 105                 110

cac cgg acc aaa atg agg cgt aag aaa cgc ttt gca aag caa ggt aac    384
His Arg Thr Lys Met Arg Arg Lys Lys Arg Phe Ala Lys Gln Gly Asn
            115                 120                 125

aaa tgg tac aag cag cac ctc tcc tac cgc ctg gtg aac tgg cct gag    432
Lys Trp Tyr Lys Gln His Leu Ser Tyr Arg Leu Val Asn Trp Pro Glu
        130                 135                 140

cat ctg ccg gag ccg gca gtt cgg ggc gcc gtg cgc gcc gcc ttc cag    480
His Leu Pro Glu Pro Ala Val Arg Gly Ala Val Arg Ala Ala Phe Gln
145                 150                 155                 160

ttg tgg agc aac gtc tca gcg ctg gag ttc tgg gag gcc cca gcc aca    528
Leu Trp Ser Asn Val Ser Ala Leu Glu Phe Trp Glu Ala Pro Ala Thr
                165                 170                 175

ggc ccc gct gac atc cgg ctc acc ttc ttc caa ggg gac cac aac gat    576
Gly Pro Ala Asp Ile Arg Leu Thr Phe Phe Gln Gly Asp His Asn Asp
                180                 185                 190

ggg ctg ggc aat gcc ttt gat ggc cca ggg ggc gcc ctg gcg cac gcc    624
Gly Leu Gly Asn Ala Phe Asp Gly Pro Gly Gly Ala Leu Ala His Ala
            195                 200                 205

ttc ctg ccc cgc cgc ggc gaa gcg cac ttc gac caa gat gag cgc tgg    672
Phe Leu Pro Arg Arg Gly Glu Ala His Phe Asp Gln Asp Glu Arg Trp
        210                 215                 220

tcc ctg agc cgc cgc cgc ggg cgc aac ctg ttc gtg gtg ctg gcg cac    720
Ser Leu Ser Arg Arg Arg Gly Arg Asn Leu Phe Val Val Leu Ala His
225                 230                 235                 240

gag atc ggt cac acg ctt ggc ctc acc cac tcg ccc gcg ccg cgc gcg    768
Glu Ile Gly His Thr Leu Gly Leu Thr His Ser Pro Ala Pro Arg Ala
                245                 250                 255

ctc atg gcg ccc tac tac aag agg ctg ggc cgc gac gcg ctg ctc agc    816
Leu Met Ala Pro Tyr Tyr Lys Arg Leu Gly Arg Asp Ala Leu Leu Ser
            260                 265                 270

tgg gac gac gtg ctg gcc gtg cag agc ctg tat ggg aag ccc cta ggg    864
Trp Asp Asp Val Leu Ala Val Gln Ser Leu Tyr Gly Lys Pro Leu Gly
            275                 280                 285

ggc tca gtg gcc gtc cag ctc cca gga aag ctg ttc act gac ttt gag    912
Gly Ser Val Ala Val Gln Leu Pro Gly Lys Leu Phe Thr Asp Phe Glu
        290                 295                 300

acc tgg gac tcc tac agc ccc caa gga agg cgc cct gaa acg cag ggc    960
Thr Trp Asp Ser Tyr Ser Pro Gln Gly Arg Arg Pro Glu Thr Gln Gly
305                 310                 315                 320

cct aaa tac tgc cac tct tcc ttc gat gcc atc act gta gac agg caa   1008
Pro Lys Tyr Cys His Ser Ser Phe Asp Ala Ile Thr Val Asp Arg Gln
                325                 330                 335

cag caa ctg tac att ttt aaa ggg agc cat ttc tgg gag gtg gca gct   1056
Gln Gln Leu Tyr Ile Phe Lys Gly Ser His Phe Trp Glu Val Ala Ala
            340                 345                 350

gat ggc aac gtc tca gag ccc cgt cca ctg cag gaa aga tgg gtc ggg   1104
Asp Gly Asn Val Ser Glu Pro Arg Pro Leu Gln Glu Arg Trp Val Gly
            355                 360                 365
```

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ctg ccc ccc aac att gag gct gcg gca gtg tca ttg aat gat gga gat      1152
Leu Pro Pro Asn Ile Glu Ala Ala Ala Val Ser Leu Asn Asp Gly Asp
    370             375                 380

ttc tac ttc ttc aaa ggg ggt cga tgc tgg agg ttc cgg ggc ccc aag      1200
Phe Tyr Phe Phe Lys Gly Gly Arg Cys Trp Arg Phe Arg Gly Pro Lys
385             390                 395                 400

cca gtg tgg ggt ctc cca cag ctg tgc cgg gca ggg ggt ctg ccc cgc      1248
Pro Val Trp Gly Leu Pro Gln Leu Cys Arg Ala Gly Gly Leu Pro Arg
                405                 410                 415

cat cct gac gcc gcc ctc ttc ttc cct cct ctg cgc cgc ctc atc ctc      1296
His Pro Asp Ala Ala Leu Phe Phe Pro Pro Leu Arg Arg Leu Ile Leu
            420                 425                 430

ttc aag ggt gcc cgc tac tac gtg ctg gcc cga ggg gga ctg caa gtg      1344
Phe Lys Gly Ala Arg Tyr Tyr Val Leu Ala Arg Gly Gly Leu Gln Val
            435                 440                 445

gag ccc tac tac ccc cga agt ctg cag gac tgg gga ggc atc cct gag      1392
Glu Pro Tyr Tyr Pro Arg Ser Leu Gln Asp Trp Gly Gly Ile Pro Glu
    450                 455                 460

gag gtc agc ggc gcc ctg ccg agg ccc gat ggc tcc atc atc ttc ttc      1440
Glu Val Ser Gly Ala Leu Pro Arg Pro Asp Gly Ser Ile Ile Phe Phe
465                 470                 475                 480

cga gat gac cgc tac tgg cgc ctc gac cag gcc aaa ctg cag gca acc      1488
Arg Asp Asp Arg Tyr Trp Arg Leu Asp Gln Ala Lys Leu Gln Ala Thr
                485                 490                 495

acc tcg ggc cgc tgg gcc acc gag ctg ccc tgg atg ggc tgc tgg cat      1536
Thr Ser Gly Arg Trp Ala Thr Glu Leu Pro Trp Met Gly Cys Trp His
            500                 505                 510

gcc aac tcg ggg agc gcc ctg ttc tga                                  1563
Ala Asn Ser Gly Ser Ala Leu Phe  *
            515                 520
```